

## SEQUENCE LISTING

<110> BURTON, Paul B. J.  
<110> DEISHER, Theresa A.

<120> COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE

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<140> -to be assigned-  
<141> 2003-08-21

<150> --to be assigned--  
<151> 2003-08-12

<150> 60/406,418  
<151> 2002-08-28

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<170> PatentIn version 3.2

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 Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu  
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cta cta ctg gag aac aat aaa aac cca acg ata aag aag aac gcc gag Leu Leu Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu 165 170 175	528
ttt gaa gat cag ggg tat tac tcc tgc gtg cat ttc ctt cat cat aat Phe Glu Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn 180 185 190	576
gga aaa cta ttt aat atc acc aaa acc ttc aat ata aca ata gtg gaa Gly Lys Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu 195 200 205	624
gat cgc agt aat ata gtt ccg gtt ctt ctt gga cca aag ctt aac cat Asp Arg Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His 210 215 220	672
gtt gca gtg gaa tta gga aaa aac gta agg ctc aac tgc tct gct ttg Val Ala Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu 225 230 235 240	720
ctg aat gaa gag gat gta att tat tgg atg ttt ggg gaa gaa aat gga Leu Asn Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Asn Gly 245 250 255	768
tcg gat cct aat ata cat gaa gag aaa gaa atg aga att atg act cca Ser Asp Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro 260 265 270	816
gaa ggc aaa tgg cat gct tca aaa gta ttg aga att gaa aat att ggt Glu Gly Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly 275 280 285	864
gaa agc aat cta aat gtt tta tat aat tgc act gtg gcc agc acg gga	912

Glu Ser Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly			
290	295	300	
ggc aca gac acc aaa agc ttc atc ttg gtg aga aaa gca gac atg gct			960
Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala			
305	310	315	320
gat atc cca ggc cac gtc ttc aca aga gga atg atc ata gct gtt ttg			1008
Asp Ile Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu			
325	330	335	
atc ttg gtg gca gta gtg tgc cta gtg act gtg tgt gtc att tat aga			1056
Ile Leu Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg			
340	345	350	
gtt gac ttg gtt cta ttt tat aga cat tta acg aga aga gat gaa aca			1104
Val Asp Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr			
355	360	365	
tta aca gat gga aaa aca tat gat gct ttt gtg tct tac cta aaa gaa			1152
Leu Thr Asp Gly Lys Thr Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu			
370	375	380	
tgc cga cct gaa aat gga gag gag cac acc ttt gct gtg gag att ttg			1200
Cys Arg Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu			
385	390	395	400
ccc agg gtg ttg gag aaa cat ttt ggg tat aag tta tgc ata ttt gaa			1248
Pro Arg Val Leu Glu Lys His Phe Gly Tyr Lys Leu Cys Ile Phe Glu			
405	410	415	
agg gat gta gtg cct gga gga gct gtt gat gaa atc cac tca ctg			1296
Arg Asp Val Val Pro Gly Gly Ala Val Val Asp Glu Ile His Ser Leu			
420	425	430	
ata gag aaa agc cga aga cta atc att gtc cta agt aaa agt tat atg			1344
Ile Glu Lys Ser Arg Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met			
435	440	445	
tct aat gag gtc agg tat gaa ctt gaa agt gga ctc cat gaa gca ttg			1392
Ser Asn Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu			
450	455	460	
gtg gaa aga aaa att aaa ata atc tta att gaa ttt aca cct gtt act			1440
Val Glu Arg Lys Ile Lys Ile Ile Leu Ile Glu Phe Thr Pro Val Thr			
465	470	475	480
gac ttc aca ttc ttg ccc caa tca cta aag ctt ttg aaa tct cac aga			1488
Asp Phe Thr Phe Leu Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg			
485	490	495	
gtt ctg aag tgg aag gcc gat aaa tct ctt tct tat aac tca agg ttc			1536
Val Leu Lys Trp Lys Ala Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe			
500	505	510	
tgg aag aac ctt ctt tac tta atg cct gca aaa aca gtc aag cca ggt			1584
Trp Lys Asn Leu Leu Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly			
515	520	525	
aga gac gaa ccg gaa gtc ttg cct gtt ctt tcc gag tct taa			1626
Arg Asp Glu Pro Glu Val Leu Pro Val Leu Ser Glu Ser			

530

535

540

<210> 6  
 <211> 541  
 <212> PRT  
 <213> Homo sapeins

<400> 6

Met Asn Cys Arg Glu Leu Pro Leu Thr Leu Trp Val Leu Ile Ser Val  
 1 5 10 15

Ser Thr Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu  
 20 25 30

Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu  
 35 40 45

Ile Glu Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu  
 50 55 60

His Val Glu Leu Asn Pro Arg Ser Ser Arg Ile Ala Leu His Asp  
 65 70 75 80

Cys Val Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr  
 85 90 95

Phe Phe Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile  
 100 105 110

Arg Arg Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys  
 115 120 125

Ile Val Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr  
 130 135 140

Tyr Gln Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys  
 145 150 155 160

Leu Leu Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu  
 165 170 175

Phe Glu Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn  
 180 185 190

Gly Lys Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu  
 195 200 205

Asp Arg Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His  
 210 215 220

Val Ala Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu  
 225 230 235 240

Leu Asn Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly  
 245 250 255

Ser Asp Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro  
 260 265 270

Glu Gly Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly  
 275 280 285  
 Glu Ser Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly  
 290 295 300  
 Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala  
 305 310 315 320  
 Asp Ile Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu  
 325 330 335  
 Ile Leu Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg  
 340 345 350  
 Val Asp Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr  
 355 360 365  
 Leu Thr Asp Gly Lys Thr Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu  
 370 375 380  
 Cys Arg Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu  
 385 390 395 400  
 Pro Arg Val Leu Glu Lys His Phe Gly Tyr Lys Leu Cys Ile Phe Glu  
 405 410 415  
 Arg Asp Val Val Pro Gly Gly Ala Val Val Asp Glu Ile His Ser Leu  
 420 425 430  
 Ile Glu Lys Ser Arg Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met  
 435 440 445  
 Ser Asn Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu  
 450 455 460  
 Val Glu Arg Lys Ile Lys Ile Ile Leu Ile Glu Phe Thr Pro Val Thr  
 465 470 475 480  
 Asp Phe Thr Phe Leu Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg  
 485 490 495  
 Val Leu Lys Trp Lys Ala Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe  
 500 505 510  
 Trp Lys Asn Leu Leu Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly  
 515 520 525  
 Arg Asp Glu Pro Glu Val Leu Pro Val Leu Ser Glu Ser  
 530 535 540

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (484)...(2283)

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cgttcagata caaaagctgg cagttactga aataaggact tgaagttcct tcctctttt	120	
ttatgtctta agagcaggaa ataaagagac agctgaaggt gtagccttga ccaactgaaa	180	
gggaaatctt catcctctga aaaaacatat gtgattctca aaaaacgcac ctggaaaatt	240	
gataaagaag cgattctgta gattctccca gcgctgttgg gctctcaatt ccttctgtga	300	
aggacaacat atggtgatgg ggaaatcaga agcttgaga ccctctacac ctggatatga	360	
atcccccttc taatacttac cagaaatgaa gggatactc agggcagagt tctgaatctc	420	
aaaacactct actctggcaa aggaatgaa ttattggagt gatgacagga acacgggaga	480	
aca atg ctc tgt ttg ggc tgg ata ttt ctt tgg ctt gtt gca gga gag	528	
Met Leu Cys Leu Gly Trp Ile Phe Leu Trp Leu Val Ala Gly Glu		
1           5                   10                   15		
cga att aaa gga ttt aat att tca ggt tgt tcc aca aaa aaa ctc ctt	576	
Arg Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu		
20                   25                           30		
tgg aca tat tct aca agg agt gaa gag gaa ttt gtc tta ttt tgt gat	624	
Trp Thr Tyr Ser Thr Arg Ser Glu Glu Phe Val Leu Phe Cys Asp		
35                   40                           45		
tta cca gag cca cag aaa tca cat ttc tgc cac aga aat cga ctc tca	672	
Leu Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser		
50                   55                           60		
cca aaa caa gtc cct gag cac ctg ccc ttc atg ggt agt aac gac cta	720	
Pro Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu		
65                   70                           75		
tct gat gtc caa tgg tac caa caa cct tcg aat gga gat cca tta gag	768	
Ser Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu		
80                   85                           90                           95		
gac att agg aaa agc tat cct cac atc att cag gac aaa tgt acc ctt	816	
Asp Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu		
100                   105                           110		
cac ttt ttg acc cca ggg gtg aat aat tct ggg tca tat att tgt aga	864	
His Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg		
115                   120                           125		
ccc aag atg att aag agc ccc tat gat gta gcc tgt tgt gtc aag atg	912	
Pro Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met		
130                   135                           140		
att tta gaa gtt aag ccc cag aca aat gca tcc tgt gag tat tcc gca	960	
Ile Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala		
145                   150                           155		
tca cat aag caa gac cta ctt ctt ggg agc act ggc tct att tct tgc	1008	
Ser His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys		
160                   165                           170                           175		

ccc agt ctc agc tgc caa agt gat gca caa agt cca gcg gta acc tgg Pro Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp 180 185 190	1056
tac aag aat gga aaa ctc ctc tct gtg gaa agg agc aac cga atc gta Tyr Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val 195 200 205	1104
gtg gat gaa gtt tat gac tat cac cag ggc aca tat gta tgt gat tac Val Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr 210 215 220	1152
act cag tcg gat act gtg agt tcg tgg aca gtc aga gct gtt gtt caa Thr Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln 225 230 235	1200
gtg aga acc att gtg gga gac act aaa ctc aaa cca gat att ctg gat Val Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp 240 245 250 255	1248
cct gtc gag gac aca ctg gaa gta gaa ctt gga aag cct tta act att Pro Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile 260 265 270	1296
agc tgc aaa gca cga ttt ggc ttt gaa agg gtc ttt aac cct gtc ata Ser Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile 275 280 285	1344
aaa tgg tac atc aaa gat tct gac cta gag tgg gaa gtc tca gta cct Lys Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro 290 295 300	1392
gag gcg aaa agt att aaa tcc act tta aag gat gaa atc att gag cgt Glu Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg 305 310 315	1440
aat atc atc ttg gaa aaa gtc act cag cgt gat ctt cgc agg aag ttt Asn Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe 320 325 330 335	1488
gtt tgc ttt gtc cag aac tcc att gga aac aca acc cag tcc gtc caa Val Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln 340 345 350	1536
ctg aaa gaa aag aga gga gtg gtg ctc ctg tac atc ctg ctt ggc acc Leu Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr 355 360 365	1584
atc ggg acc ctg gtg gcc gtg ctg gcg agt gcc ctc ctc tac agg Ile Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg 370 375 380	1632
cac tgg att gaa ata gtg ctg ctg tac cgg acc tac cag agc aag gat His Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp 385 390 395	1680
cag acg ctt ggg gat aaa aag gat ttt gat gct ttc gta tcc tat gca Gln Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala 400 405 410 415	1728

aaa tgg agc tct ttt cca agt gag gcc act tca tct ctg agt gaa gaa Lys Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu 420 425 430	1776
cac ttg gcc ctg agc cta ttt cct gat gtt tta gaa aac aaa tat gga His Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly 435 440 445	1824
tat agc ctg tgt ttg ctt gaa aga gat gtg gct cca gga gga gtg tat Tyr Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr 450 455 460	1872
gca gaa gac att gtg agc att att aag aga agc aga aga gga ata ttt Ala Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe 465 470 475	1920
atc ttg agc ccc aac tat gtc aat gga ccc agt atc ttt gaa cta caa Ile Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln 480 485 490 495	1968
gca gca gtg aat ctt gcc ttg gat gat caa aca ctg aaa ctc att tta Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu 500 505 510	2016
att aag ttc tgt tac ttc caa gag cca gag tct cta cct cat ctc gtg Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val 515 520 525	2064
aaa aaa gct ctc agg gtt ttg ccc aca gtt act tgg aga ggc tta aaa Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys 530 535 540	2112
tca gtt cct ccc aat tct agg ttc tgg gcc aaa atg cgc tac cac atg Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met 545 550 555	2160
cct gtg aaa aac tct cag gga ttc acg tgg aac cag ctc aga att acc Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr 560 565 570 575	2208
tct agg att ttt cag tgg aaa gga ctc agt aga aca gaa acc act ggg Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly 580 585 590	2256
agg agc tcc cag cct aag gaa tgg tga aatgaggcct ggagccccct Arg Ser Ser Gln Pro Lys Glu Trp 595	2303
ccagtccagt ccctggata gagatgtgc tggacagaac tcacagctct gtgtgtgtgt	2363
gttcaggctg atagaaatt caaagagtct cctgccagca ccaagcaagc ttgatggaca	2423
atggaatggg attgagactg tggtttagag ccttgattt cctggactgg acagacggcg	2483
agtgaattct ctagaccttg ggtactttca gtacacaaca cccctaagat ttcccagtgg	2543
tccgagcaga atcagaaaaat acagctactt ctgccttatg gctaggaaac tgtcatgtct	2603
accatgtatt gtacatatga ctttatgtat acttgcaatc aaataaatat tattttatta	2663
aaaaaaaaac cggaattc	2681

<210> 8  
<211> 599  
<212> PRT  
<213> Homo sapiens

<400> 8

Met Leu Cys Leu Gly Trp Ile Phe Leu Trp Leu Val Ala Gly Glu Arg  
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Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu Trp  
20 25 30

Thr Tyr Ser Thr Arg Ser Glu Glu Phe Val Leu Phe Cys Asp Leu  
35 40 45

Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro  
50 55 60

Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser  
65 70 75 80

Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp  
85 90 95

Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His  
100 105 110

Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro  
115 120 125

Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile  
130 135 140

Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser  
145 150 155 160

His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro  
165 170 175

Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr  
180 185 190

Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val  
195 200 205

Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr  
210 215 220

Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val  
225 230 235 240

Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro  
245 250 255

Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser  
260 265 270

Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys

275	280	285
Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu		
290	295	300
Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn		
305	310	315
Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe Val		
325	330	335
Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln Leu		
340	345	350
Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile		
355	360	365
Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His		
370	375	380
Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp Gln		
385	390	395
Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys		
405	410	415
Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His		
420	425	430
Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr		
435	440	445
Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala		
450	455	460
Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile		
465	470	475
Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala		
485	490	495
Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu Ile		
500	505	510
Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val Lys		
515	520	525
Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser		
530	535	540
Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro		
545	550	555
Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser		
565	570	575
Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly Arg		
580	585	590
Ser Ser Gln Pro Lys Glu Trp		
595		

<210> 9  
 <211> 644  
 <212> DNA  
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<220>  
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 <222> (66)...(599)

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tgacc atg aga cac aac tgg aca cca gac ctc agc cct ttg tgg gtc ctg 110  
 Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val Leu  
 1 5 10 15

ctc ctg tgt gcc cac gtc gtc act ctc ctg gtc aga gcc aca cct gtc 158  
 Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro Val  
 20 25 30

tcg cag acc acc aca gct gcc act gcc tca gtt aga agc aca aag gac 206  
 Ser Gln Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys Asp  
 35 40 45

ccc tgc ccc tcc cag ccc cca gtg ttc cca gca gct aag cag tgt cca 254  
 Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys Pro  
 50 55 60

gca ttg gaa gtg acc tgg cca gag gtg gaa gtg cca ctg aat gga acg 302  
 Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly Thr  
 65 70 75

ctg agc tta tcc tgt gtg gcc tgc agc cgc ttc ccc aac ttc agc atc 350  
 Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser Ile  
 80 85 90 95

ctc tac tgg ctg ggc aat ggt tcc ttc att gag cac ctc cca ggc cga 398  
 Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly Arg  
 100 105 110

ctg tgg gag ggg agc acc agc cgg gaa cgt ggg agc aca ggt acg cag 446  
 Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr Gln  
 115 120 125

ctg tgc aag gcc ttg gtg ctg gag cag ctg acc cct gcc ctg cac agc 494  
 Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His Ser  
 130 135 140

acc aac ttc tcc tgt gtg ctc gtg gac cct gaa cag gtt gtc cag cgt 542  
 Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln Arg  
 145 150 155

cac gtc gtc ctg gcc cag ctc tgg gct ggg ctg agg gca acc ttg ccc 590  
 His Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu Pro  
 160 165 170 175

ccc acc caa gaagccctgc cctccagcca cagcagtcca cagcagcagg gttaa 644  
 Pro Thr Gln

<210> 10

<211> 178

<212> PRT

<213> Homo sapiens

<400> 10

Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val Leu Leu  
1 5 10 15

Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro Val Ser  
20 25 30

Gln Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys Asp Pro  
35 40 45

Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys Pro Ala  
50 55 60

Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly Thr Leu  
65 70 75 80

Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser Ile Leu  
85 90 95

Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly Arg Leu  
100 105 110

Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr Gln Leu  
115 120 125

Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His Ser Thr  
130 135 140

Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln Arg His  
145 150 155 160

Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu Pro Pro  
165 170 175

Thr Gln

<210> 11

<211> 422

<212> PRT

<213> Homo sapiens

<400> 11

Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val Leu Leu  
1 5 10 15

Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro Val Ser  
20 25 30

Gln Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys Asp Pro

35	40	45	
Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys Pro Ala			
50	55	60	
Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly Thr Leu			
65	70	75	80
Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser Ile Leu			
85	90	95	
Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly Arg Leu			
100	105	110	
Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr Gln Leu			
115	120	125	
Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His Ser Thr			
130	135	140	
Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln Arg His			
145	150	155	160
Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu Pro Pro			
165	170	175	
Thr Gln Glu Ala Leu Pro Ser Ser His Ser Ser Pro Gln Gln Gln Gly			
180	185	190	
Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
195	200	205	
Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
210	215	220	
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
225	230	235	240
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
245	250	255	
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			
260	265	270	
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp			
275	280	285	
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro			
290	295	300	
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu			
305	310	315	320
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn			
325	330	335	
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile			
340	345	350	
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr			
355	360	365	

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
370 375 380

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
385 390 395 400

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
405 410 415

Ser Leu Ser Pro Gly Lys  
420

<210> 12  
<211> 579  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(579)

<220>  
<221> sig\_peptide  
<222> (1)..(108)

<220>  
<221> mat\_peptide  
<222> (109)..()

<400> 12  
atg gct gct gaa cca gta gaa gac aat tgc atc aac ttt gtg gca atg 48  
Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met  
-35 -30 -25

aaa ttt att gac aat acg ctt tac ttt ata gct gaa gat gat gaa aac 96  
Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn  
-20 -15 -10 -5

ctg gaa tca gat tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata 144  
Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile  
-1 1 5 10

aga aat ttg aat gac caa gtt ctc ttc att gac caa gga aat cgg cct 192  
Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro  
15 20 25

cta ttt gaa gat atg act gat tct gac tgt aga gat aat gca ccc cgg 240  
Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg  
30 35 40

acc ata ttt att ata agt atg tat aaa gat agc cag cct aga ggt atg 288  
Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met  
45 50 55 60

gct gta act atc tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt 336  
Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys  
65 70 75

gag aac aaa att att tcc ttt aag gaa atg aat cct cct gat aac atc Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile 80 85 90	384
aag gat aca aaa agt gac atc ata ttc ttt cag aga agt gtc cca gga Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly 95 100 105	432
cat gat aat aag atg caa ttt gaa tct tca tca tac gaa gga tac ttt His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe 110 115 120	480
cta gct tgt gaa aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys 125 130 135 140	528
gag gat gaa ttg ggg gat aga tct ata atg ttc act gtt caa aac gaa Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu 145 150 155	576
gac Asp	579

<210> 13  
<211> 193  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (73)..(73)  
<223> The 'Xaa' at location 73 stands for Thr, or Ile.

<400> 13

Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met  
-35 -30 -25

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn  
-20 -15 -10 -5

Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile  
-1 1 5 10

Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro  
15 20 25

Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg  
30 35 40

Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met  
45 50 55 60

Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys  
65 70 75

Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile  
80 85 90

Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly  
95 100 105

His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe  
110 115 120

Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys  
125 130 135 140

Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu  
145 150 155

Asp

<210> 14  
<211> 157  
<212> PRT  
<213> Homo sapiens

<400> 14

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn  
1 5 10 15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile  
65 70 75 80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys  
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys  
100 105 110

Met Gln Phe Glu Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu  
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu  
130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp  
145 150 155

<210> 15  
<211> 765  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS  
<222> (4)..(765)

<400> 15  
gtc atg gaa tac gcc tct gac gct tca ctg gac ccc gaa gcc ccg tgg 48  
Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp  
1 5 10 15  
  
cct ccc gcg ccc cgc gct cgc gcc tgc cgc gta ctg cct tgg gcc ctg 96  
Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu  
20 25 30  
  
gtc gcg ggg ctg ctg ctg ctg ctc gct gcc gcc tgc gcc gtc 144  
Val Ala Gly Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val  
35 40 45  
  
ttc ctc gcc tgc ccc tgg gcc gtg tcc ggg gct cgc gcc tcg ccc ggc 192  
Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly  
50 55 60  
  
tcc gcg gcc agc ccg aga ctc cgc gag ggt ccc gag ctt tcg ccc gac 240  
Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp  
65 70 75  
  
gat ccc gcc ggc ctc ttg gac ctg cgg cag ggc atg ttt gcg cag ctg 288  
Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu  
80 85 90 95  
  
gtg gcc caa aat gtt ctg ctg atc gat ggg ccc ctg agc tgg tac agt 336  
Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser  
100 105 110  
  
gac cca ggc ctg gca ggc gtg tcc ctg acg ggg ggc ctg agc tac aaa 384  
Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Leu Ser Tyr Lys  
115 120 125  
  
gag gac acg aag gag ctg gtg gtc aag gct gga gtc tac tat gtc 432  
Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val  
130 135 140  
  
ttc ttt caa cta gag ctg cgg cgc gtg gtg gcc ggc gag ggc tca ggc 480  
Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly  
145 150 155  
  
tcc gtt tca ctt gcg ctg cac ctg cag cca ctg cgc tct gct gct ggg 528  
Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly  
160 165 170 175  
  
gcc gcc gcc ctg gct ttg acc gtg gac ctg cca ccc gcc tcc tcc gag 576  
Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu  
180 185 190  
  
gct cgg aac tcg gcc ttc ggt ttc cag ggc cgc ttg ctg cac ctg agt 624  
Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser  
195 200 205  
  
gcc ggc cag cgc ctg ggc gtc cat ctt cac act gag gcc agg gca cgc 672  
Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg  
210 215 220  
  
cat gcc tgg cag ctt acc cag ggc gcc aca gtc ttg gga ctc ttc cgg 720

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg			
225	230	235	
gtg acc ccc gaa atc cca gcc gga ctc cct tca ccg agg tcg gaa			765
Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu			
240	245	250	
<210> 16			
<211> 254			
<212> PRT			
<213> Homo sapiens			
<400> 16			
Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro			
1	5	10	15
Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val			
20	25	30	
Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe			
35	40	45	
Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser			
50	55	60	
Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp			
65	70	75	80
Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val			
85	90	95	
Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp			
100	105	110	
Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu			
115	120	125	
Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe			
130	135	140	
Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser			
145	150	155	160
Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala			
165	170	175	
Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala			
180	185	190	
Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala			
195	200	205	
Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His			
210	215	220	
Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val			
225	230	235	240
Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu			

<210> 17  
 <211> 1415  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (120)..(884)

<220>  
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 <222> (120)..(189)

<220>  
 <221> mat\_peptide  
 <222> (189)..()

<400> 17  
 agtggaaaat tctccggcag ccctgagatc tcaagagtga catttgttag accagctaat 60  
 ttgattaaaa ttctcttggaa atcagcttg ctagtatcat acctgtgcca gatttcatc 119  
 atg gga aac agc tgt tac aac ata gta gcc act ctg ttg ctg gtc ctc 167  
 Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu  
 -20 -15 -10  
 aac ttt gag agg aca aga tca ttg cag gat cct tgt agt aac tgc cca 215  
 Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro  
 -5 -1 1 5  
 gct ggt aca ttc tgt gat aat aac agg aat cag att tgc agt ccc tgt 263  
 Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
 10 15 20 25  
 cct cca aat agt ttc tcc agc gca ggt gga caa agg acc tgt gac ata 311  
 Pro Pro Asn Ser Phe Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
 30 35 40  
 tgc agg cag tgt aaa ggt gtt ttc agg acc agg aag gag tgt tcc tcc 359  
 Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
 45 50 55  
 acc agc aat gca gag tgt gac tgc act cca ggg ttt cac tgc ctg ggg 407  
 Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
 60 65 70  
 gca gga tgc agc atg tgt gaa cag gat tgt aaa caa ggt caa gaa ctg 455  
 Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu  
 75 80 85  
 aca aaa aaa ggt tgt aaa gac tgt tgc ttt ggg aca ttt aac gat cag 503  
 Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln  
 90 95 100 105  
 aaa cgt ggc atc tgt cga ccc tgg aca aac tgt tct ttg gat gga aag 551  
 Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys  
 110 115 120

tct gtg ctt gtg aat ggg acg aag gag agg gac gtg gtc tgt gga cca	599		
Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro			
125	130	135	
tct cca gcc gac ctc tct ccg gga gca tcc tct gtg acc ccg cct gcc	647		
Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala			
140	145	150	
cct gcg aga gag cca gga cac tct ccg cag atc atc tcc ttc ttt ctt	695		
Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu			
155	160	165	
gcg ctg acg tcg act gcg ttg ctc ttc ctg ctg ttc ttc ctc acg ctc	743		
Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu			
170	175	180	185
cgt ttc tct gtt gtt aaa cgg ggc aga aag aaa ctc ctg tat ata ttc	791		
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe			
190	195	200	
aaa caa cca ttt atg aga cca gta caa act act caa gag gaa gat ggc	839		
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly			
205	210	215	
tgt agc tgc cga ttt cca gaa gaa gaa gaa gga tgt gaa ctg	884		
Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu			
220	225	230	
tgaaatggaa gtcaataggg ctgttggac tttcttgaaa agaagcaagg aaatatgagt	944		
catccgctat cacagtttc aaaagcaaga acaccatcct acataataacc caggattccc	1004		
ccaaacacacg ttctttcta aatgccaatg agttggcctt taaaaatgca ccacttttt	1064		
ttttttttt gacagggctc cactctgtca cccaggctgg agtgcagtgg caccaccatg	1124		
gctctctgca gccttgacct ctgggagctc aagtgtatcct cctgcctcag tctccttagta	1184		
gctggaaacta caaggaaggg ccaccacacc tgactaactt ttttgtttt tgtttggtaa	1244		
agatggcatt tcgccatgtt gtacaggctg gtctcaaact ccttaggtca ctttggcctc	1304		
ccaaagtgct gggattacag acatgaactg ccaggccccgg ccaaataat gcaccacttt	1364		
taacagaaca gacagatgag gacagagctg gtgataaaaa aaaaaaaaaa a	1415		

<210> 18  
 <211> 255  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu  
 -20 -15 -10

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro  
 -5 -1 1 5

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
 10 15 20 25  
 Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
 30 35 40  
 Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
 45 50 55  
 Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
 60 65 70  
 Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu  
 75 80 85  
 Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln  
 90 95 100 105  
 Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys  
 110 115 120  
 Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro  
 125 130 135  
 Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala  
 140 145 150  
 Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu  
 155 160 165  
 Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu  
 170 175 180 185  
 Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe  
 190 195 200  
 Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly  
 205 210 215  
 Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu  
 220 225 230

<210> 19  
 <211> 648  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(645)  
 <400> 19  
 atg cat gtg ccg gcg ggc tcc gtg gcc agc cac ctg ggg acc acg agc  
 Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser  
 1 5 10 15

48

cgc agc tat ttc tat ttg acc aca gcc act ctg gct ctg tgc ctt gtc  
 Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val  
 20 25 30

96

ttc acg gtg gcc act att atg gtg ttg gtc gtt cag agg acg gac tcc Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser 35 40 45	144
att ccc aac tca cct gac aac gtc ccc ctc aaa gga gga aat tgc tca Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser 50 55 60	192
gaa gac ctc tta tgt atc ctg aaa aga gct cca ttc aag aag tca tgg Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp 65 70 75 80	240
gcc tac ctc caa gtg gca aag cat cta aac aaa acc aag ttg tct tgg Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp 85 90 95	288
aac aaa gat ggc att ctc cat gga gtc aga tat cag gat ggg aat ctg Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu 100 105 110	336
gtg atc caa ttc cct ggt ttg tac ttc atc att tgc caa ctg cag ttt Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe 115 120 125	384
ctt gta caa tgc cca aat aat tct gtc gat ctg aag ttg gag ctt ctc Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu 130 135 140	432
atc aac aag cat atc aaa aaa cag gcc ctg gtg aca gtg tgt gag tct Ile Asn Lys His Ile Lys Gln Ala Leu Val Thr Val Cys Glu Ser 145 150 155 160	480
gga atg caa acg aaa cac gta tac cag aat ctc tct caa ttc ttg ctg Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu 165 170 175	528
gat tac ctg cag gtc aac acc acc ata tca gtc aat gtg gat aca ttc Asp Tyr Leu Gln Val Asn Thr Ile Ser Val Asn Val Asp Thr Phe 180 185 190	576
cag tac ata gat aca agc acc ttt cct ctt gag aat gtg ttg tcc atc Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile 195 200 205	624
ttc tta tac agt aat tca gac tga Phe Leu Tyr Ser Asn Ser Asp 210 215	648

<210> 20  
<211> 215  
<212> PRT  
<213> Homo sapiens

<400> 20

Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly Thr Thr Ser  
1 5 10 15

Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu Cys Leu Val

20

25

30

Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg Thr Asp Ser  
 35 40 45

Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly Asn Cys Ser  
 50 55 60

Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp  
 65 70 75 80

Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp  
 85 90 95

Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu  
 100 105 110

Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe  
 115 120 125

Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu  
 130 135 140

Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser  
 145 150 155 160

Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu  
 165 170 175

Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe  
 180 185 190

Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile  
 195 200 205

Phe Leu Tyr Ser Asn Ser Asp  
 210 215

<210> 21

<211> 705

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(702)

<400> 21

atg gac cca ggg ctg cag caa gca ctc aac gga atg gcc cct cct gga 48  
 Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly  
 1 5 10 15

gac aca gcc atg cat gtg ccg gcg ggc tcc gtg gcc agc cac ctg ggg 96  
 Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly  
 20 25 30

acc acg agc cgc agc tat ttc tat ttg acc aca gcc act ctg gct ctg 144  
 Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu  
 35 40 45

tgc ctt gtc ttc acg gtg gcc act att atg gtc ttg gtc gtt cag agg	192
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg	
50 55 60	
acg gac tcc att ccc aac tca cct gac aac gtc ccc ctc aaa gga gga	240
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly	
65 70 75 80	
aat tgc tca gaa gac ctc tta tgt atc ctg aaa aga gct cca ttc aag	288
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys	
85 90 95	
aag tca tgg gcc tac ctc caa gtg gca aag cat cta aac aaa acc aag	336
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys	
100 105 110	
ttg tct tgg aac aaa gat ggc att ctc cat gga gtc aga tat cag gat	384
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp	
115 120 125	
ggg aat ctg gtg atc caa ttc cct ggt ttg tac ttc atc att tgc caa	432
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln	
130 135 140	
ctg cag ttt ctt gta caa tgc cca aat aat tct gtc gat ctg aag ttg	480
Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu	
145 150 155 160	
gag ctt ctc atc aac aag cat atc aaa aaa cag gcc ctg gtg aca gtg	528
Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val	
165 170 175	
tgt gag tct gga atg caa acg aaa cac gta tac cag aat ctc tct caa	576
Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln	
180 185 190	
ttc ttg ctg gat tac ctg cag gtc aac acc acc ata tca gtc aat gtg	624
Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val	
195 200 205	
gat aca ttc cag tac ata gat aca agc acc ttt cct ctt gag aat gtg	672
Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val	
210 215 220	
ttg tcc atc ttc tta tac agt aat tca gac tga	705
Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp	
225 230	

<210> 22  
 <211> 234  
 <212> PRT  
 <213> Homo sapiens  
 <400> 22

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly  
 1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly

20

25

30

Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu  
 35 40 45

Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg  
 50 55 60

Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly  
 65 70 75 80

Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys  
 85 90 95

Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys  
 100 105 110

Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp  
 115 120 125

Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln  
 130 135 140

Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu  
 145 150 155 160

Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val  
 165 170 175

Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln  
 180 185 190

Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val  
 195 200 205

Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val  
 210 215 220

Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp  
 225 230

<210> 23

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1785)

<400> 23

atg cgc gtc ctc ctc gcc gcg ctg gga ctg ctg ttc ctg ggg gcg cta  
 Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu  
 1 5 10 15

48

cga gcc ttc cca cag gat cga ccc ttc gag gac acc tgt cat gga aac  
 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn  
 20 25 30

96

ccc agc cac tac tat gac aag gct gtc agg agg tgc tgt tac cgc tgc Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys 35 40 45	144
ccc atg ggg ctg ttc ccg aca cag cag tgc cca cag agg cct act gac Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp 50 55 60	192
tgc agg aag cag tgt gag cct gac tac tac ctg gat gag gcc gac cgc Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg 65 70 75 80	240
tgt aca gcc tgc gtg act tgt tct cga gat gac ctc gtg gag aag acg Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr 85 90 95	288
ccg tgt gca tgg aac tcc tcc cgt gtc tgc gaa tgt cga ccc ggc atg Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met 100 105 110	336
ttc tgt tcc acg tct gcc gtc aac tcc tgt gcc cgc tgc ttc ttc cat Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His 115 120 125	384
tct gtc tgt ccg gca ggg atg att gtc aag ttc cca ggc acg gcg cag Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln 130 135 140	432
aag aac acg gtc tgt gag ccg gct tcc cca ggg gtc agc cct gcc tgt Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys 145 150 155 160	480
gcc agc cca gag aac tgc aag gaa ccc tcc agt ggc acc atc ccc cag Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln 165 170 175	528
gcc aag ccc acc ccg gtg tcc cca gca acc tcc agt gcc agc acc atg Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met 180 185 190	576
cct gta aga ggg ggc acc cgc ctc gcc cag gaa gct gct tct aaa ctg Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu 195 200 205	624
acg agg gct ccc gac tct ccc tcc tct gtg gga agg cct agt tca gat Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp 210 215 220	672
cca ggt ctg tcc cca aca cag cca tgc cca gag ggg tct ggt gat tgc Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys 225 230 235 240	720
aga aag cag tgt gag ccc gac tac tac ctg gac gag gcc ggc cgc tgc Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys 245 250 255	768
aca gcc tgc gtg agc tgt tct cga gat gac ctt gtg gag aag acg cca Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro 260 265 270	816
tgt gca tgg aac tcc tcc cgc acc tgc gaa tgt cga cct ggc atg atc	864

Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile			
275	280	285	
tgt gcc aca tca gcc acc aac tcc tgt gcc cgc tgt gtc ccc tac cca			912
Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro			
290	295	300	
atc tgt gca gga gag acg gtc acc aag ccc cag gat atg gct gag aag			960
Ile Cys Ala Gly Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys			
305	310	315	320
gac acc acc ttt gag gcg cca ccc ctg ggg acc cag ccg gac tgc aac			1008
Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn			
325	330	335	
ccc acc cca gag aat ggc gag gcg cct gcc agc acc agc ccc act cag			1056
Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln			
340	345	350	
agc ttg ctg gtg gac tcc cag gcc agt aag acg ctg ccc atc cca acc			1104
Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr			
355	360	365	
agc gct ccc gtc gct ctc tcc acg ggg aag ccc gtt ctg gat gca			1152
Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala			
370	375	380	
ggg cca gtg ctc ttc tgg gtg atc ctg gtg ttg gtt gtg gtc ggc			1200
Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Gly			
385	390	395	400
tcc agc gcc ttc ctc ctg tgc cac cgg agg gcc tgc agg aag cga att			1248
Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile			
405	410	415	
cgg cag aag ctc cac ctg tac ccg gtc cag acc tcc cag ccc aag			1296
Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys			
420	425	430	
cta gag ctt gtg gat tcc aga ccc agg agg agc tca acg cag ctg agg			1344
Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg			
435	440	445	
agt ggt gcg tcg gtg aca gaa ccc gtc gcg gaa gag cga ggg tta atg			1392
Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met			
450	455	460	
agc cag cca ctg atg gag acc tgc cac agc gtg ggg gca gcc tac ctg			1440
Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu			
465	470	475	480
gag agc ctg ccg ctg cag gat gcc agc ccg gcc ggg ggc ccc tcg tcc			1488
Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser			
485	490	495	
ccc agg gac ctt cct gag ccc cgg gtg tcc acg gag cac acc aat aac			1536
Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn			
500	505	510	
aag att gag aaa atc tac atc atg aag gct gac acc gtg atc gtg ggg			1584
Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly			

515	520	525	
acc gtg aag gct gag ctg ccg gag ggc cg <sup>g</sup> ggc ctg g <sup>c</sup> ggg cca gca Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala			1632
530	535	540	
gag ccc gag ttg gag gag gag ctg gag g <sup>c</sup> gac cat acc ccc cac tac Glu Pro Glu Leu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr			1680
545	550	555	560
ccc gag cag gag aca gaa ccg cct ctg ggc agc tgc agc gat gtc atg Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met			1728
565	570	575	
ctc tca gtg gaa gag gaa ggg aaa gaa gac ccc ttg ccc aca gct gcc Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala			1776
580	585	590	
tct gga aag tga Ser Gly Lys			1788
595			
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<211> 595			
<212> PRT			
<213> Homo sapiens			
<400> 24			
Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu			
1	5	10	15
Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn			
20	25	30	
Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys			
35	40	45	
Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp			
50	55	60	
Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg			
65	70	75	80
Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr			
85	90	95	
Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met			
100	105	110	
Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His			
115	120	125	
Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln			
130	135	140	
Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys			
145	150	155	160
Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln			

165	170	175
Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met		
180	185	190
Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu		
195	200	205
Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp		
210	215	220
Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys		
225	230	235
Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys		
245	250	255
Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro		
260	265	270
Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile		
275	280	285
Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro		
290	295	300
Ile Cys Ala Gly Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys		
305	310	315
Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn		
325	330	335
Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln		
340	345	350
Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr		
355	360	365
Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala		
370	375	380
Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Val Gly		
385	390	395
400		
Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile		
405	410	415
Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys		
420	425	430
Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg		
435	440	445
Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met		
450	455	460
Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu		
465	470	475
480		
Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser		
485	490	495

Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn  
500 505 510

Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly  
515 520 525

Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala  
530 535 540

Glu Pro Glu Leu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr  
545 550 555 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met  
565 570 575

Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala  
580 585 590

Ser Gly Lys  
595

<210> 25

<211> 696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138) .. (686)

<400> 25

ggccctggga ccttcgccta ttttctgatt gataggctt gttttgtctt taccccttc 60

tttctgggga aaacttcagt tttatcgac gttccccc ttccatatctt catcttccct 120

ctacccagat tgtgaag atg gaa agg gtc caa ccc ctg gaa gag aat gtg 170  
Met Glu Arg Val Gln Pro Leu Glu Asn Val  
1 5 10

gga aat gca gcc agg cca aga ttc gag agg aac aag cta ttg ctg gtg 218  
Gly Asn Ala Ala Arg Pro Arg Phe Glu Arg Asn Lys Leu Leu Val  
15 20 25

gcc tct gta att cag gga ctg ggg ctg ctc ctg tgc ttc acc tac atc 266  
Ala Ser Val Ile Gln Gly Leu Gly Leu Leu Cys Phe Thr Tyr Ile  
30 35 40

tgc ctg cac ttc tct gct ctt cag gta tca cat cgg tat cct cga att 314  
Cys Leu His Phe Ser Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile  
45 50 55

caa agt atc aaa gta caa ttt acc gaa tat aag aag gag aaa ggt ttc 362  
Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe  
60 65 70 75

atc ctc act tcc caa aag gag gat gaa atc atg aag gtg cag aac aac 410  
Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn  
80 85 90

tca gtc atc atc aac tgt gat ggg ttt tat ctc atc tcc ctg aag ggc Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly	458
95 100 105	
tac ttc tcc cag gaa gtc aac att agc ctt cat tac cag aag gat gag Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu	506
110 115 120	
gag ccc ctc ttc caa ctg aag aag gtc agg tct gtc aac tcc ttg atg Glu Pro Leu Phe Gln Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met	554
125 130 135	
gtg gcc tct ctg act tac aaa gac aaa gtc tac ttg aat gtg acc act Val Ala Ser Leu Thr Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr	602
140 145 150 155	
gac aat acc tcc ctg gat gac ttc cat gtg aat ggc gga gaa ctg att Asp Asn Thr Ser Leu Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile	650
160 165 170	
cct atc cat caa aat cct ggt gaa ttc tgt gtc ctt tgagggcctg Leu Ile His Gln Asn Pro Gly Glu Phe Cys Val Leu	696
175 180	

<210> 26  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 26

Met Glu Arg Val Gln Pro Leu Glu Glu Asn Val Gly Asn Ala Ala Arg 1 5 10 15	
Pro Arg Phe Glu Arg Asn Lys Leu Leu Leu Val Ala Ser Val Ile Gln 20 25 30	
Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser 35 40 45	
Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val 50 55 60	
Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln 65 70 75 80	
Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn 85 90 95	
Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu 100 105 110	
Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln 115 120 125	
Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr 130 135 140	
Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu	

145	150	155	160
Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn			
165	170	175	
Pro Gly Glu Phe Cys Val Leu			
180			
<210> 27			
<211> 865			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (15) .. (845)			
<400> 27			
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Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro			
1	5	10	50
tgt gcg gct ctg ctc ctg ggc ctg ggg ctg agc acc gtg acg ggg			
Cys Ala Ala Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly			
15	20	25	98
ctc cac tgt gtc ggg gac acc tac ccc agc aac gac cgg tgc tgc cac			
Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His			
30	35	40	146
gag tgc agg cca ggc aac ggg atg gtg agc cgc tgc agc cgc tcc cag			
Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln			
45	50	55	60
aac acg gtg tgc cgt cgc tgc ggg ccg ggc ttc tac aac gac gtg gtc			
Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val			
65	70	75	242
agc tcc aag ccg tgc aag ccc tgc acg tgg tgt aac ctc aga agt ggg			
Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly			
80	85	90	290
agt gag cgg aag cag ctg tgc acg gcc aca cag gac aca gtc tgc cgc			
Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg			
95	100	105	338
tgc cgg ggc acc cag ccc ctg gac agc tac aag cct gga gtt gac			
Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp			
110	115	120	386
tgt gcc ccc tgc cct cca ggg cac ttc tcc cca ggc gac aac cag gcc			
Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala			
125	130	135	140
tgc aag ccc tgg acc aac tgc acc ttg gct ggg aag cac acc ctg cag			
Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln			
145	150	155	482
ccg gcc agc aat agc tcg gac gca atc tgt gag gac agg gac ccc cca			
			530

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro			
160	165	170	
gcc acg cag ccc cag gag acc cag ggc ccc ccg gcc agg ccc atc act			578
Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr			
175	180	185	
gtc cag ccc act gaa gcc tgg ccc aga acc tca cag gga ccc tcc acc			626
Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr			
190	195	200	
cgg ccc gtg gag gtc ccc ggg ggc cgt gcg gtt gcc gcc atc ctg ggc			674
Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly			
205	210	215	220
ctg ggc ctg gtg ctg ggg ctg ctg ggc ccc ctg gcc atc ctg ctg gcc			722
Leu Gly Leu Val Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala			
225	230	235	
ctg tac ctg ctc cgg agg gac cag agg ctg ccc ccc gat gcc cac aag			770
Leu Tyr Leu Leu Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys			
240	245	250	
ccc cct ggg gga ggc agt ttc cgg acc ccc atc caa gag gag cag gcc			818
Pro Pro Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala			
255	260	265	
gac gcc cac tcc acc ctg gcc aag atc tgacctggc ccaccaaggt			865
Asp Ala His Ser Thr Leu Ala Lys Ile			
270	275		

<210> 28  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 28

Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu			
1	5	10	15
Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val			
20	25	30	
Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro			
35	40	45	
Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys			
50	55	60	
Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro			
65	70	75	80
Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys			
85	90	95	
Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly			
100	105	110	
Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys			

115	120	125
Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp		
130	135	140
Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn		
145	150	155
160		
Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro		
165	170	175
Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr		
180	185	190
Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu		
195	200	205
Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val		
210	215	220
Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu		
225	230	235
240		
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly		
245	250	255
Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser		
260	265	270
Thr Leu Ala Lys Ile		
275		

<210> 29  
 <211> 1599  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (67)..(1596)

<400> 29  
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 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser  
 1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156  
 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile  
 15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aaa gca ttg cca gaa aac 204  
 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252  
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val 65 70 75	300
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe 80 85 90	348
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu 95 100 105 110	396
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val 115 120 125	444
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu 130 135 140	492
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn 145 150 155	540
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu 160 165 170	588
ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser 175 180 185 190	636
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln 195 200 205	684
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr 210 215 220	732
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln 225 230 235	780
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu 240 245 250	828
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile 255 260 265 270	876
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly 275 280 285	924
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr 290 295 300	972

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt		1020	
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly			
305	310	315	
att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac		1068	
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn			
320	325	330	
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg		1116	
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu			
335	340	345	350
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg		1164	
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val			
355	360	365	
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg		1212	
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val			
370	375	380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa		1260	
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys			
385	390	395	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt		1308	
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe			
400	405	410	
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca		1356	
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr			
415	420	425	430
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc		1404	
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser			
435	440	445	
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc		1452	
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile			
450	455	460	
cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc		1500	
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val			
465	470	475	
ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata		1548	
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile			
480	485	490	
ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta		1596	
Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val			
495	500	505	510
tag		1599	

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 <211> 510  
 <212> PRT  
 <213> Homo sapiens

<400> 30

Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn  
 1 5 10 15

Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu  
 20 25 30

Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
 180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
 195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
 210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
 225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
 245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
 260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
 275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
 290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
 305 310 315 320

Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser
325									330				335		
Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro
340								345				350			
Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys
355								360				365			
Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu
370				375						380					
Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser
385								390		395			400		
Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly
	405							410					415		
Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	
		420					425					430			
Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala
		435					440				445				
Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala
		450				455				460					
Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	Phe	Leu
		465				470				475				480	
Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	Gly	Leu
								485		490			495		
Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val		
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Asp Tyr Lys Asp Asp Asp Lys  
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1 5 10

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<211> 9  
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1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser  
20 25